

4-32761A\_UNZ.ST25.txt  
SEQUENCE LISTING

<110> Novartis AG

<120> Organic Compound

<130> 4-32761P1/UNZ

<160> 44

<170> PatentIn version 3.1

<210> 1

<211> 18

<212> PRT

<213> Rattus norvegicus

<220>

<221> PEPTIDE

<222> (1)..(18)

<223> rat NogoA\_623-640

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Glu Ala

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<212> PRT

<213> Mus musculus

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<221> CHAIN

<222> (1)..(221)

<223> Variable part of Heavy Chain of 11C7 with leader sequence

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Gly Gly Ser Leu Lys Leu Ser Cys Val Val Ser Gly Phe Asp Phe Arg  
35 40 45

Arg Asn Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu  
50 55 60

Trp Ile Gly Glu Ile Asn Pro Asp Ser Ser Lys Ile Asn Tyr Thr Pro  
65 70 75 80

Ser Leu Lys Asp Lys Phe Ile Ile Ser Arg Asp Asn Ala Lys Asn Thr  
85 90 95

Leu Tyr Leu Gln Val Ser Thr Val Arg Ser Glu Asp Thr Ala Leu Tyr  
100 105 110

Tyr Cys Val Arg Pro Val Trp Met Tyr Ala Met Asp Tyr Trp Gly Gln  
115 120 125

Gly Thr Ser Val Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Ser Val  
130 135 140

Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val Thr  
145 150 155 160

Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Val Thr  
165 170 175

Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala Val  
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<211> 238

<212> PRT

<213> Mus musculus

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<221> CHAIN

<222> (1)..(238)

<223> Light Chain of 11C7 with leader sequence

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Thr Ile Gly Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu  
 35 40 45

Leu His Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Arg Pro  
 50 55 60

Gly Gln Ser Pro Lys Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser  
 65 70 75 80

Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr  
 85 90 95

Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Leu Tyr Tyr Cys  
 100 105 110

Trp Gln Gly Thr His Phe Pro Gln Thr Phe Gly Gly Gly Thr Lys Leu  
 115 120 125

Glu Ile Lys Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro  
 130 135 140

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Ser Ser Glu Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu  
 145 150 155 160  
 Asn Asn Phe Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly  
 165 170 175  
 Ser Glu Arg Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser  
 180 185 190  
 Lys Asp Ser Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp  
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<213> Homo sapiens

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<221> CDS

<222> (1)..(3579)

<223> Human NogoA

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Pro Arg Pro Gln Pro Ala Phe Lys Tyr Gln Phe Val Arg Glu Pro Glu	
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gac gag gag gaa gaa gag gag gag gaa gag gag gac gag gac gaa gac	144
Asp Glu Glu Glu Glu Glu Glu Glu Glu Glu Asp Glu Asp Glu Asp	
35 40 45	
ctg gag gag ctg gag gtg ctg gag agg aag ccc gcc gcc ggg ctg tcc	192
Leu Glu Glu Leu Glu Val Leu Glu Arg Lys Pro Ala Ala Gly Leu Ser	
50 55 60	
gcg gcc cca gtg ccc acc gcc cct gcc gcc ggc gcg ccc ctg atg gac	240
Page 4	

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Ala 65	Ala	Pro	Val	Pro	Thr 70	Ala	Pro	Ala	Ala	Gly 75	Ala	Pro	Leu	Met	Asp 80	
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gct Ala	ccc Pro	ccc Pro	gtc Val 100	gcc Ala	ccg Pro	gag Glu	cgg Arg	cag Gln 105	ccg Pro	tct Ser	tgg Trp	gac Asp 110	ccg Pro 110	agc Ser	ccg Pro	336
gtg Val	tcg Ser	tcg Ser 115	acc Thr	gtg Val	ccc Pro	gcg Ala	cca Pro 120	tcc Ser	ccg Pro	ctg Leu	tct Ser	gct Ala 125	gcc Ala	gca Ala	gtc Val	384
tcg Ser	ccc Pro 130	tcc Ser	aag Lys	ctc Leu	cct Pro	gag Glu 135	gac Asp	gac Asp	gag Glu	cct Pro	ccg Pro 140	gcc Ala	cgg Arg	cct Pro	ccc Pro	432
cct Pro 145	cct Pro	ccc Pro	ccg Pro	gcc Ala	agc Ser 150	gtg Val	agc Ser	ccc Pro	cag Gln 155	gca Ala 155	gag Glu	ccc Pro	gtg Val	tgg Trp	acc Thr 160	480
ccg Pro	cca Pro	gcc Ala	ccg Pro	gct Ala 165	ccc Pro	gcc Ala	gcg Ala	ccc Pro	ccc Pro 170	tcc Ser	acc Thr	ccg Pro	gcc Ala	gcg Ala 175	ccc Pro	528
aag Lys	cgc Arg	agg Arg	ggc Gly 180	tcc Ser	tcg Ser	ggc Gly	tca Ser	gtg Val 185	gat Asp	gag Glu	acc Thr	ctt Leu	ttt Phe 190	gct Ala	ctt Leu	576
cct Pro	gct Ala	gca Ala 195	tct Ser	gag Glu	cct Pro	gtg Val	ata Ile 200	cgc Arg	tcc Ser	tct Ser	gca Ala	gaa Glu 205	aat Asn	atg Met	gac Asp	624
ttg Leu	aag Lys 210	gag Glu	cag Gln	cca Pro	ggt Gly	aac Asn 215	act Thr	att Ile	tcg Ser	gct Ala	ggt Gly 220	caa Gln	gag Glu	gat Asp	ttc Phe	672
cca Pro 225	tct Ser	gtc Val	ctg Leu	ctt Leu	gaa Glu 230	act Thr	gct Ala	gct Ala	tct Ser	ctt Leu 235	cct Pro	tct Ser	ctg Leu	tct Ser	cct Pro 240	720
ctc Leu	tca Ser	gcc Ala	gct Ala	tct Ser 245	ttc Phe	aaa Lys	gaa Glu	cat His	gaa Glu 250	tac Tyr	ctt Leu	ggt Gly	aat Asn	ttg Leu 255	tca Ser	768
aca Thr	gta Val	tta Leu	ccc Pro 260	act Thr	gaa Glu	gga Gly	aca Thr	ctt Leu 265	caa Gln	gaa Glu	aat Asn	gtc Val	agt Ser 270	gaa Glu	gct Ala	816
tct Ser	aaa Lys	gag Glu 275	gtc Val	tca Ser	gag Glu	aag Lys	gca Ala 280	aaa Lys	act Thr	cta Leu	ctc Leu	ata Ile 285	gat Asp	aga Arg	gat Asp	864
tta Leu	aca Thr 290	gag Glu	ttt Phe	tca Ser	gaa Glu	tta Leu 295	gaa Glu	tac Tyr	tca Ser	gaa Glu	atg Met 300	gga Gly	tca Ser	tcg Ser	ttc Phe	912
agt Ser 305	gtc Val	tct Ser	cca Pro	aaa Lys	gca Ala 310	gaa Glu	tct Ser	gcc Ala	gta Val	ata Ile 315	gta Val	gca Ala	aat Asn	cct Pro	agg Arg 320	960

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gaa Glu	gaa Glu	ata Ile	atc Ile	gtg Val 325	aaa Lys	aat Asn	aaa Lys	gat Asp	gaa Glu 330	gaa Glu	gag Glu	aag Lys	tta Leu	gtt Val 335	agt Ser	1008
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ttg Leu	gtt Val	aaa Lys 355	gag Glu	gat Asp	gaa Glu	gtt Val	gtg Val 360	tct Ser	tca Ser	gaa Glu	aaa Lys	gca Ala 365	aaa Lys	gac Asp	agt Ser	1104
ttt Phe	aat Asn 370	gaa Glu	aag Lys	aga Arg	gtt Val	gca Ala 375	gtg Val	gaa Glu	gct Ala	cct Pro	atg Met 380	agg Arg	gag Glu	gaa Glu	tat Tyr	1152
gca Ala 385	gac Asp	ttc Phe	aaa Lys	cca Pro	ttt Phe 390	gag Glu	cga Arg	gta Val	tgg Trp	gaa Glu 395	gtg Val	aaa Lys	gat Asp	agt Ser	aag Lys 400	1200
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gaa Glu	agt Ser	aaa Lys	gtg Val 420	gat Asp	aaa Lys	aaa Lys	tgt Cys	ttt Phe 425	gca Ala	gat Asp	agc Ser	ctt Leu	gag Glu 430	caa Gln	act Thr	1296
aat Asn	cac His	gaa Glu 435	aaa Lys	gat Asp	agt Ser	gag Glu	agt Ser 440	agt Ser	aat Asn	gat Asp	gat Asp	act Thr 445	tct Ser	ttc Phe	ccc Pro	1344
agt Ser	acg Thr 450	cca Pro	gaa Glu	ggt Gly	ata Ile	aag Lys 455	gat Asp	cgt Arg	tca Ser	gga Gly	gca Ala 460	tat Tyr	atc Ile	aca Thr	tgt Cys	1392
gct Ala 465	ccc Pro	ttt Phe	aac Asn	cca Pro	gca Ala 470	gca Ala	act Thr	gag Glu	agc Ser	att Ile 475	gca Ala	aca Thr	aac Asn	att Ile	ttt Phe 480	1440
cct Pro	ttg Leu	tta Leu	gga Gly	gat Asp 485	cct Pro	act Thr	tca Ser	gaa Glu	aat Asn 490	aag Lys	acc Thr	gat Asp	gaa Glu	aaa Lys 495	aaa Lys	1488
ata Ile	gaa Glu	gaa Glu	aag Lys 500	aag Lys	gcc Ala	caa Gln	ata Ile	gta Val 505	aca Thr	gag Glu	aag Lys	aat Asn	act Thr 510	agc Ser	acc Thr	1536
aaa Lys	aca Thr	tca Ser 515	aac Asn	cct Pro	ttt Phe	ctt Leu	gta Val 520	gca Ala	gca Ala	cag Gln	gat Asp	tct Ser 525	gag Glu	aca Thr	gat Asp	1584
tat Tyr	gtc Val 530	aca Thr	aca Thr	gat Asp	aat Asn	tta Leu 535	aca Thr	aag Lys	gtg Val	act Thr	gag Glu 540	gaa Glu	gtc Val	gtg Val	gca Ala	1632
aac Asn 545	atg Met	cct Pro	gaa Glu	ggc Gly	ctg Leu 550	act Thr	cca Pro	gat Asp	tta Leu	gta Val 555	cag Gln	gaa Glu	gca Ala	tgt Cys	gaa Glu 560	1680
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Met Asp Leu Val 580 Gln Thr Ser Glu Val 585 Met Gln Glu Ser Leu Tyr Pro	
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cca gtt ttg cct gac att gtt atg gaa gca cca ttg aat tct gca gtt	1872
Pro Val 610 Leu Pro Asp Ile Val 615 Met Glu Ala Pro Leu 620 Asn Ser Ala Val	
cct agt gct ggt gct tcc gtg ata cag ccc agc tca tca cca tta gaa	1920
Pro Ser 625 Ala Gly Ala Ser 630 Val Ile Gln Pro Ser 635 tca tca cca tta gaa	
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Ala Ser Ser Val 645 Asn Tyr Glu Ser Ile Lys 650 His Glu Pro Glu Asn 655 Pro	
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Ile Lys Glu 675 Glu Ile Lys Glu Pro 680 Glu Asn Ile Asn Ala 685 Ala Leu Gln	
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Glu Thr 690 Glu Ala Pro Tyr Ile Ser Ile Ala Cys Asp 700 Leu Ile Lys Glu	
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Thr Lys Leu Ser Ala Glu 710 Pro Ala Pro Asp Phe 715 Ser Asp Tyr Ser Glu 720	
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Met Ala Lys Val 725 Glu Gln Pro Val Pro 730 Asp His Ser Glu Leu Val 735 Glu	
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Asp Ser Ser Pro 740 Asp Ser Glu Pro Val 745 Asp Leu Phe Ser Asp 750 Asp Ser	
ata cct gac gtt cca caa aaa caa gat gaa act gtg atg ctt gtg aaa	2304
Ile Pro Asp 755 Val Pro Gln Lys Gln 760 Asp Glu Thr Val Met 765 Leu Val Lys	
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Glu Ser 770 Leu Thr Glu Thr Ser 775 Phe Glu Ser Met Ile 780 Glu Tyr Glu Asn	
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Lys Glu Lys Leu Ser Ala 790 Leu Pro Pro Glu Gly 795 Gly Lys Pro Tyr Leu 800	
gaa tct ttt aag ctc agt tta gat aac aca aaa gat acc ctg tta cct	2448
Glu Ser Phe Lys Leu Ser Leu Asp Asn Thr 810 Lys Asp Thr Leu Leu 815 Pro	
gat gaa gtt tca aca ttg agc aaa aag gag aaa att cct ttg cag atg	2496
Asp Glu Val Ser Thr Leu Ser Lys Lys Glu Lys Ile Pro Leu Gln Met	

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aag	gaa	gca	cag	ata	aga	gaa	act	gaa	acg	ttt	tca	gat	tca	tct	cca	2592													
Lys	Glu	Ala	Gln	Ile	Arg	Glu	Thr	Glu	Thr	Phe	Ser	Asp	Ser	Ser	Pro														
	850					855					860																		
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Ser	Glu	Glu	Leu	Val	Gln	Lys	Tyr	Ser	Asn	Ser	Ala	Leu	Gly	His	
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Val	Asn	Cys	Thr	Ile	Lys	Glu	Leu	Arg	Arg	Leu	Phe	Leu	Val	Asp	
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gat	tta	gtt	gat	tct	ctg	aag	ttt	gca	gtg	ttg	atg	tgg	gta	ttt	3384
Asp	Leu	Val	Asp	Ser	Leu	Lys	Phe	Ala	Val	Leu	Met	Trp	Val	Phe	
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aaa	gat	gct	atg	gct	aaa	atc	caa	gca	aaa	atc	cct	gga	ttg	aag	3564
Lys	Asp	Ala	Met	Ala	Lys	Ile	Gln	Ala	Lys	Ile	Pro	Gly	Leu	Lys	
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Arg	Lys	Ala	Glu												
1190															
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Asp Glu Glu Glu Glu Glu Glu Glu Glu Glu Asp Glu Asp Glu Asp  
35 40 45

Leu Glu Glu Leu Glu Val Leu Glu Arg Lys Pro Ala Ala Gly Leu Ser  
50 55 60

Ala Ala Pro Val Pro Thr Ala Pro Ala Ala Gly Ala Pro Leu Met Asp  
65 70 75 80

Phe Gly Asn Asp Phe Val Pro Pro Ala Pro Arg Gly Pro Leu Pro Ala  
85 90 95

Ala Pro Pro Val Ala Pro Glu Arg Gln Pro Ser Trp Asp Pro Ser Pro  
100 105 110

Val Ser Ser Thr Val Pro Ala Pro Ser Pro Leu Ser Ala Ala Ala Val  
115 120 125

Ser Pro Ser Lys Leu Pro Glu Asp Asp Glu Pro Pro Ala Arg Pro Pro  
130 135 140

Pro Pro Pro Pro Ala Ser Val Ser Pro Gln Ala Glu Pro Val Trp Thr  
145 150 155 160

Pro Pro Ala Pro Ala Pro Ala Ala Pro Pro Ser Thr Pro Ala Ala Pro  
165 170 175

Lys Arg Arg Gly Ser Ser Gly Ser Val Asp Glu Thr Leu Phe Ala Leu  
180 185 190

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195 200 205

Leu Lys Glu Gln Pro Gly Asn Thr Ile Ser Ala Gly Gln Glu Asp Phe  
210 215 220

Pro Ser Val Leu Leu Glu Thr Ala Ala Ser Leu Pro Ser Leu Ser Pro  
225 230 235 240

Leu Ser Ala Ala Ser Phe Lys Glu His Glu Tyr Leu Gly Asn Leu Ser  
245 250 255

Thr Val Leu Pro Thr Glu Gly Thr Leu Gln Glu Asn Val Ser Glu Ala  
260 265 270

Ser Lys Glu Val Ser Glu Lys Ala Lys Thr Leu Leu Ile Asp Arg Asp  
 275 280 285  
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 290 295 300  
 Ser Val Ser Pro Lys Ala Glu Ser Ala Val Ile Val Ala Asn Pro Arg  
 305 310 315 320  
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 Phe Asn Glu Lys Arg Val Ala Val Glu Ala Pro Met Arg Glu Glu Tyr  
 370 375 380  
 Ala Asp Phe Lys Pro Phe Glu Arg Val Trp Glu Val Lys Asp Ser Lys  
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 Glu Asp Ser Asp Met Leu Ala Ala Gly Gly Lys Ile Glu Ser Asn Leu  
 405 410 415  
 Glu Ser Lys Val Asp Lys Lys Cys Phe Ala Asp Ser Leu Glu Gln Thr  
 420 425 430  
 Asn His Glu Lys Asp Ser Glu Ser Ser Asn Asp Asp Thr Ser Phe Pro  
 435 440 445  
 Ser Thr Pro Glu Gly Ile Lys Asp Arg Ser Gly Ala Tyr Ile Thr Cys  
 450 455 460  
 Ala Pro Phe Asn Pro Ala Ala Thr Glu Ser Ile Ala Thr Asn Ile Phe  
 465 470 475 480  
 Pro Leu Leu Gly Asp Pro Thr Ser Glu Asn Lys Thr Asp Glu Lys Lys  
 485 490 495  
 Ile Glu Glu Lys Lys Ala Gln Ile Val Thr Glu Lys Asn Thr Ser Thr  
 500 505 510  
 Lys Thr Ser Asn Pro Phe Leu Val Ala Ala Gln Asp Ser Glu Thr Asp  
 515 520 525

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Tyr Val Thr Thr Asp Asn Leu Thr Lys Val Thr Glu Glu Val Val Ala  
 530 535 540  
 Asn Met Pro Glu Gly Leu Thr Pro Asp Leu Val Gln Glu Ala Cys Glu  
 545 550 555 560  
 Ser Glu Leu Asn Glu Val Thr Gly Thr Lys Ile Ala Tyr Glu Thr Lys  
 565 570 575  
 Met Asp Leu Val Gln Thr Ser Glu Val Met Gln Glu Ser Leu Tyr Pro  
 580 585 590  
 Ala Ala Gln Leu Cys Pro Ser Phe Glu Glu Ser Glu Ala Thr Pro Ser  
 595 600 605  
 Pro Val Leu Pro Asp Ile Val Met Glu Ala Pro Leu Asn Ser Ala Val  
 610 615 620  
 Pro Ser Ala Gly Ala Ser Val Ile Gln Pro Ser Ser Ser Pro Leu Glu  
 625 630 635 640  
 Ala Ser Ser Val Asn Tyr Glu Ser Ile Lys His Glu Pro Glu Asn Pro  
 645 650 655  
 Pro Pro Tyr Glu Glu Ala Met Ser Val Ser Leu Lys Lys Val Ser Gly  
 660 665 670  
 Ile Lys Glu Glu Ile Lys Glu Pro Glu Asn Ile Asn Ala Ala Leu Gln  
 675 680 685  
 Glu Thr Glu Ala Pro Tyr Ile Ser Ile Ala Cys Asp Leu Ile Lys Glu  
 690 695 700  
 Thr Lys Leu Ser Ala Glu Pro Ala Pro Asp Phe Ser Asp Tyr Ser Glu  
 705 710 715 720  
 Met Ala Lys Val Glu Gln Pro Val Pro Asp His Ser Glu Leu Val Glu  
 725 730 735  
 Asp Ser Ser Pro Asp Ser Glu Pro Val Asp Leu Phe Ser Asp Asp Ser  
 740 745 750  
 Ile Pro Asp Val Pro Gln Lys Gln Asp Glu Thr Val Met Leu Val Lys  
 755 760 765  
 Glu Ser Leu Thr Glu Thr Ser Phe Glu Ser Met Ile Glu Tyr Glu Asn  
 770 775 780

Lys Glu Lys Leu Ser Ala Leu Pro Pro Glu Gly Gly Lys Pro Tyr Leu  
785 790 795 800

Glu Ser Phe Lys Leu Ser Leu Asp Asn Thr Lys Asp Thr Leu Leu Pro  
805 810 815

Asp Glu Val Ser Thr Leu Ser Lys Lys Glu Lys Ile Pro Leu Gln Met  
820 825 830

Glu Glu Leu Ser Thr Ala Val Tyr Ser Asn Asp Asp Leu Phe Ile Ser  
835 840 845

Lys Glu Ala Gln Ile Arg Glu Thr Glu Thr Phe Ser Asp Ser Ser Pro  
850 855 860

Ile Glu Ile Ile Asp Glu Phe Pro Thr Leu Ile Ser Ser Lys Thr Asp  
865 870 875 880

Ser Phe Ser Lys Leu Ala Arg Glu Tyr Thr Asp Leu Glu Val Ser His  
885 890 895

Lys Ser Glu Ile Ala Asn Ala Pro Asp Gly Ala Gly Ser Leu Pro Cys  
900 905 910

Thr Glu Leu Pro His Asp Leu Ser Leu Lys Asn Ile Gln Pro Lys Val  
915 920 925

Glu Glu Lys Ile Ser Phe Ser Asp Asp Phe Ser Lys Asn Gly Ser Ala  
930 935 940

Thr Ser Lys Val Leu Leu Leu Pro Pro Asp Val Ser Ala Leu Ala Thr  
945 950 955 960

Gln Ala Glu Ile Glu Ser Ile Val Lys Pro Lys Val Leu Val Lys Glu  
965 970 975

Ala Glu Lys Lys Leu Pro Ser Asp Thr Glu Lys Glu Asp Arg Ser Pro  
980 985 990

Ser Ala Ile Phe Ser Ala Glu Leu Ser Lys Thr Ser Val Val Asp Leu  
995 1000 1005

Leu Tyr Trp Arg Asp Ile Lys Lys Thr Gly Val Val Phe Gly Ala  
1010 1015 1020

Ser Leu Phe Leu Leu Leu Ser Leu Thr Val Phe Ser Ile Val Ser  
Page 13

1025

1030

1035

Val Thr Ala Tyr Ile Ala Leu Ala Leu Leu Ser Val Thr Ile Ser  
1040 1045 1050

Phe Arg Ile Tyr Lys Gly Val Ile Gln Ala Ile Gln Lys Ser Asp  
1055 1060 1065

Glu Gly His Pro Phe Arg Ala Tyr Leu Glu Ser Glu Val Ala Ile  
1070 1075 1080

Ser Glu Glu Leu Val Gln Lys Tyr Ser Asn Ser Ala Leu Gly His  
1085 1090 1095

Val Asn Cys Thr Ile Lys Glu Leu Arg Arg Leu Phe Leu Val Asp  
1100 1105 1110

Asp Leu Val Asp Ser Leu Lys Phe Ala Val Leu Met Trp Val Phe  
1115 1120 1125

Thr Tyr Val Gly Ala Leu Phe Asn Gly Leu Thr Leu Leu Ile Leu  
1130 1135 1140

Ala Leu Ile Ser Leu Phe Ser Val Pro Val Ile Tyr Glu Arg His  
1145 1150 1155

Gln Ala Gln Ile Asp His Tyr Leu Gly Leu Ala Asn Lys Asn Val  
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Arg Lys Ala Glu  
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<211> 18

<212> PRT

<213> Homo sapiens

<220>

<221> PEPTIDE

<222> (1)..(18)

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 1 5 10 15

Glu Ala

&lt;210&gt; 7

&lt;211&gt; 819

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; PEPTIDE

&lt;222&gt; (1)..(819)

&lt;223&gt; human Nig

&lt;400&gt; 7

Asp Glu Thr Leu Phe Ala Leu Pro Ala Ala Ser Glu Pro Val Ile Arg  
 1 5 10 15

Ser Ser Ala Glu Asn Met Asp Leu Lys Glu Gln Pro Gly Asn Thr Ile  
 20 25 30

Ser Ala Gly Gln Glu Asp Phe Pro Ser Val Leu Leu Glu Thr Ala Ala  
 35 40 45

Ser Leu Pro Ser Leu Ser Pro Leu Ser Ala Ala Ser Phe Lys Glu His  
 50 55 60

Glu Tyr Leu Gly Asn Leu Ser Thr Val Leu Pro Thr Glu Gly Thr Leu  
 65 70 75 80

Gln Glu Asn Val Ser Glu Ala Ser Lys Glu Val Ser Glu Lys Ala Lys  
 85 90 95

Thr Leu Leu Ile Asp Arg Asp Leu Thr Glu Phe Ser Glu Leu Glu Tyr  
 100 105 110

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Ser Glu Met Gly Ser Ser Phe Ser Val Ser Pro Lys Ala Glu Ser Ala  
115 120 125

Val Ile Val Ala Asn Pro Arg Glu Glu Ile Ile Val Lys Asn Lys Asp  
130 135 140

Glu Glu Glu Lys Leu Val Ser Asn Asn Ile Leu His Asn Gln Gln Glu  
145 150 155 160

Leu Pro Thr Ala Leu Thr Lys Leu Val Lys Glu Asp Glu Val Val Ser  
165 170 175

Ser Glu Lys Ala Lys Asp Ser Phe Asn Glu Lys Arg Val Ala Val Glu  
180 185 190

Ala Pro Met Arg Glu Glu Tyr Ala Asp Phe Lys Pro Phe Glu Arg Val  
195 200 205

Trp Glu Val Lys Asp Ser Lys Glu Asp Ser Asp Met Leu Ala Ala Gly  
210 215 220

Gly Lys Ile Glu Ser Asn Leu Glu Ser Lys Val Asp Lys Lys Cys Phe  
225 230 235 240

Ala Asp Ser Leu Glu Gln Thr Asn His Glu Lys Asp Ser Glu Ser Ser  
245 250 255

Asn Asp Asp Thr Ser Phe Pro Ser Thr Pro Glu Gly Ile Lys Asp Arg  
260 265 270

Ser Gly Ala Tyr Ile Thr Cys Ala Pro Phe Asn Pro Ala Ala Thr Glu  
275 280 285

Ser Ile Ala Thr Asn Ile Phe Pro Leu Leu Gly Asp Pro Thr Ser Glu  
290 295 300

Asn Lys Thr Asp Glu Lys Lys Ile Glu Glu Lys Lys Ala Gln Ile Val  
305 310 315 320

Thr Glu Lys Asn Thr Ser Thr Lys Thr Ser Asn Pro Phe Leu Val Ala  
325 330 335

Ala Gln Asp Ser Glu Thr Asp Tyr Val Thr Thr Asp Asn Leu Thr Lys  
340 345 350

Val Thr Glu Glu Val Val Ala Asn Met Pro Glu Gly Leu Thr Pro Asp  
355 360 365



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Leu Val Gln Glu Ala Cys Glu Ser Glu Leu Asn Glu Val Thr Gly Thr  
 370 375 380  
 Lys Ile Ala Tyr Glu Thr Lys Met Asp Leu Val Gln Thr Ser Glu Val  
 385 390 400  
 Met Gln Glu Ser Leu Tyr Pro Ala Ala Gln Leu Cys Pro Ser Phe Glu  
 405 410 415  
 Glu Ser Glu Ala Thr Pro Ser Pro Val Leu Pro Asp Ile Val Met Glu  
 420 425 430  
 Ala Pro Leu Asn Ser Ala Val Pro Ser Ala Gly Ala Ser Val Ile Gln  
 435 440 445  
 Pro Ser Ser Ser Pro Leu Glu Ala Ser Ser Val Asn Tyr Glu Ser Ile  
 450 455 460  
 Lys His Glu Pro Glu Asn Pro Pro Pro Tyr Glu Glu Ala Met Ser Val  
 465 470 475 480  
 Ser Leu Lys Lys Val Ser Gly Ile Lys Glu Glu Ile Lys Glu Pro Glu  
 485 490 495  
 Asn Ile Asn Ala Ala Leu Gln Glu Thr Glu Ala Pro Tyr Ile Ser Ile  
 500 505 510  
 Ala Cys Asp Leu Ile Lys Glu Thr Lys Leu Ser Ala Glu Pro Ala Pro  
 515 520 525  
 Asp Phe Ser Asp Tyr Ser Glu Met Ala Lys Val Glu Gln Pro Val Pro  
 530 535 540  
 Asp His Ser Glu Leu Val Glu Asp Ser Ser Pro Asp Ser Glu Pro Val  
 545 550 555 560  
 Asp Leu Phe Ser Asp Asp Ser Ile Pro Asp Val Pro Gln Lys Gln Asp  
 565 570 575  
 Glu Thr Val Met Leu Val Lys Glu Ser Leu Thr Glu Thr Ser Phe Glu  
 580 585 590  
 Ser Met Ile Glu Tyr Glu Asn Lys Glu Lys Leu Ser Ala Leu Pro Pro  
 595 600 605  
 Glu Gly Gly Lys Pro Tyr Leu Glu Ser Phe Lys Leu Ser Leu Asp Asn  
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610

615

Thr Lys Asp Thr Leu Leu Pro Asp Glu Val Ser Thr Leu Ser Lys Lys  
625 630 635 640

Glu Lys Ile Pro Leu Gln Met Glu Glu Leu Ser Thr Ala Val Tyr Ser  
645 650 655

Asn Asp Asp Leu Phe Ile Ser Lys Glu Ala Gln Ile Arg Glu Thr Glu  
660 665 670

Thr Phe Ser Asp Ser Ser Pro Ile Glu Ile Ile Asp Glu Phe Pro Thr  
675 680 685

Leu Ile Ser Ser Lys Thr Asp Ser Phe Ser Lys Leu Ala Arg Glu Tyr  
690 695 700

Thr Asp Leu Glu Val Ser His Lys Ser Glu Ile Ala Asn Ala Pro Asp  
705 710 715 720

Gly Ala Gly Ser Leu Pro Cys Thr Glu Leu Pro His Asp Leu Ser Leu  
725 730 735

Lys Asn Ile Gln Pro Lys Val Glu Glu Lys Ile Ser Phe Ser Asp Asp  
740 745 750

Phe Ser Lys Asn Gly Ser Ala Thr Ser Lys Val Leu Leu Leu Pro Pro  
755 760 765

Asp Val Ser Ala Leu Ala Thr Gln Ala Glu Ile Glu Ser Ile Val Lys  
770 775 780

Pro Lys Val Leu Val Lys Glu Ala Glu Lys Lys Leu Pro Ser Asp Thr  
785 790 795 800

Glu Lys Glu Asp Arg Ser Pro Ser Ala Ile Phe Ser Ala Glu Leu Ser  
805 810 815

Lys Thr Ser

<210> 8

<211> 10

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<213> Mus musculus

<220>

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<222> (1)..(10)

<223> hypervariable part of heavy chain of 11C7

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<210> 9

<211> 17

<212> PRT

<213> Mus musculus

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<222> (1)..(17)

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<210> 10

<211> 9

<212> PRT

<213> Mus musculus

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<213> Mus musculus

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<223> hypervariable part of light chain of 11C7

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Lys Ser Ser Gln Ser Leu Leu His Ser Asp Gly Lys Thr Tyr Leu Asn  
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<210> 12

<211> 7

<212> PRT

<213> Mus musculus

<220>

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<222> (1)..(7)

<223> hypervariable part of light chain of 11C7

<400> 12

Leu Val Ser Lys Leu Asp Ser  
1 5

&lt;210&gt; 13

&lt;211&gt; 9

&lt;212&gt; PRT

&lt;213&gt; Mus musculus

&lt;220&gt;

&lt;221&gt; BINDING

&lt;222&gt; (1)..(9)

&lt;223&gt; hypervariable part of light chain of 11C7

&lt;400&gt; 13

Trp Gln Gly Thr His Phe Pro Gln Thr  
 1 5

&lt;210&gt; 14

&lt;211&gt; 30

&lt;212&gt; DNA

&lt;213&gt; Mus musculus

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; (1)..(30)

&lt;223&gt; DNA-CDR1-11C7

&lt;400&gt; 14

ggattcgatt ttagaagaaa ttggatgagt

30

&lt;210&gt; 15

&lt;211&gt; 51

&lt;212&gt; DNA

&lt;213&gt; Mus musculus

&lt;220&gt;

&lt;221&gt; misc\_binding

<222> (1)..(51)

<223> DNA-CDR2-11C7

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<210> 16

<211> 27

<212> DNA

<213> Mus musculus

<220>

<221> misc\_binding

<222> (1)..(27)

<223> DNA-CDR3-11C7

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<210> 17

<211> 48

<212> DNA

<213> Mus musculus

<220>

<221> misc\_binding

<222> (1)..(48)

<223> DNA-CDR'1-11C7

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<210> 18

<211> 21

<212> DNA

<213> Mus musculus

<220>

<221> misc\_binding

<222> (1)..(21)

<223> DNA-CDR'2-11C7

<400> 18

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21

<210> 19

<211> 27

<212> DNA

<213> Mus musculus

<220>

<221> misc\_binding

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<223> DNA-CDR'3-11C7

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27

<210> 20

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<212> DNA

<213> Mus musculus

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<221> CDS

<222> (1)..(54)

<223> leader sequence for heavy chain of 11C7

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<400> 20  
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 Met Asp Phe Gly Leu Ile Phe Phe Ile Val Gly Leu Leu Lys Gly Val  
 1 5 10 15

cag tgt 54  
 Gln Cys

<210> 21

<211> 18

<212> PRT

<213> Mus musculus

<400> 21

Met Asp Phe Gly Leu Ile Phe Phe Ile Val Gly Leu Leu Lys Gly Val  
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Gln Cys

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<211> 57

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (1)..(57)

<223> leader sequence for 11C7-light chain

<400> 22  
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 Met Ser Pro Ala Gln Phe Leu Phe Leu Leu Val Leu Trp Ile Arg Glu  
 1 5 10 15

acc agc ggt 57  
 Thr Ser Gly

<210> 23



&lt;211&gt; 19

&lt;212&gt; PRT

&lt;213&gt; Mus musculus

&lt;400&gt; 23

Met Ser Pro Ala Gln Phe Leu Phe Leu Leu Val Leu Trp Ile Arg Glu  
 1 5 10 15

Thr Ser Gly

&lt;210&gt; 24

&lt;211&gt; 181

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; PEPTIDE

&lt;222&gt; (1)..(181)

&lt;223&gt; human Nig-D20

&lt;400&gt; 24

Gly Thr Lys Ile Ala Tyr Glu Thr Lys Met Asp Leu Val Gln Thr Ser  
 1 5 10 15

Glu Val Met Gln Glu Ser Leu Tyr Pro Ala Ala Gln Leu Cys Pro Ser  
 20 25 30

Phe Glu Glu Ser Glu Ala Thr Pro Ser Pro Val Leu Pro Asp Ile Val  
 35 40 45

Met Glu Ala Pro Leu Asn Ser Ala Val Pro Ser Ala Gly Ala Ser Val  
 50 55 60

Ile Gln Pro Ser Ser Ser Pro Leu Glu Ala Ser Ser Val Asn Tyr Glu  
 65 70 75 80

Ser Ile Lys His Glu Pro Glu Asn Pro Pro Pro Tyr Glu Glu Ala Met  
 85 90 95

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Ser Val Ser Leu Lys Lys Val Ser Gly Ile Lys Glu Glu Ile Lys Glu  
100 105 110  
Pro Glu Asn Ile Asn Ala Ala Leu Gln Glu Thr Glu Ala Pro Tyr Ile  
115 120 125  
Ser Ile Ala Cys Asp Leu Ile Lys Glu Thr Lys Leu Ser Ala Glu Pro  
130 135 140  
Ala Pro Asp Phe Ser Asp Tyr Ser Glu Met Ala Lys Val Glu Gln Pro  
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Val Pro Asp His Ser Glu Leu Val Glu Asp Ser Ser Pro Asp Ser Glu  
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Pro Val Asp Leu Phe  
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<210> 25

<211> 3492

<212> DNA

<213> Rattus norvegicus

<220>

<221> CDS

<222> (1)..(3492)

<223> rat NogoA

<400> 25

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Met Glu Asp Ile Asp Gln Ser Ser Leu Val Ser Ser Ser Thr Asp Ser  
1 5 10 15

ccg ccc cgg cct ccg ccc gcc ttc aag tac cag ttc gtg acg gag ccc 96  
Pro Pro Arg Pro Pro Pro Ala Phe Lys Tyr Gln Phe Val Thr Glu Pro  
20 25 30

gag gac gag gag gac gag gag gag gag gac gag gag gag gac gac 144  
Glu Asp Glu Glu Asp Glu Glu Glu Glu Glu Asp Glu Glu Glu Asp Asp  
35 40 45

gag gac cta gag gaa ctg gag gtg ctg gag agg aag ccc gca gcc ggg 192  
Glu Asp Leu Glu Glu Leu Glu Val Leu Glu Arg Lys Pro Ala Ala Gly  
50 55 60

ctg tcc gca gct gcg gtg ccg ccc gcc gcc gcc gcg ccg ctg ctg gac 240  
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Leu 65	Ser	Ala	Ala	Ala	Val 70	Pro	Pro	Ala	Ala	Ala 75	Ala	Pro	Leu	Leu	Asp 80	
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Phe	Ser	Ser	Asp	Ser 85	Val	Pro	Pro	Ala	Pro 90	Arg	Gly	Pro	Leu	Pro 95	Ala	
gcg	ccc	cct	gcc	gct	cct	gag	agg	cag	cca	tcc	tgg	gaa	cgc	agc	ccc	336
Ala	Pro	Pro	Ala 100	Ala	Pro	Glu	Arg	Gln 105	Pro	Ser	Trp	Glu	Arg 110	Ser	Pro	
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Ala	Ala	Pro 115	Ala	Pro	Ser	Leu	Pro 120	Pro	Ala	Ala	Ala	Val 125	Leu	Pro	Ser	
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Lys	Leu 130	Pro	Glu	Asp	Asp	Glu 135	Pro	Pro	Ala	Arg	Pro 140	Pro	Pro	Pro	Pro	
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Pro	Ala	Gly	Ala	Ser	Pro 150	Leu	Ala	Glu	Pro	Ala 155	Ala	Pro	Pro	Ser	Thr 160	
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Phe	Ala	Leu	Pro 180	Ala	Ala	Ser	Glu	Pro 185	Val	Ile	Pro	Ser	Ser 190	Ala	Glu	
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Lys	Ile	Met 195	Asp	Leu	Met	Glu	Gln 200	Pro	Gly	Asn	Thr	Val 205	Ser	Ser	Gly	
caa	gag	gat	ttc	cca	tct	gtc	ctg	ctt	gaa	act	gct	gcc	tct	ctt	cct	672
Gln	Glu	Asp	Phe	Pro	Ser	Val 215	Leu	Leu	Glu	Thr	Ala 220	Ala	Ser	Leu	Pro	
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Ser	Leu	Ser	Pro	Leu	Ser 230	Thr	Val	Ser	Phe	Lys 235	Glu	His	Gly	Tyr	Leu 240	
ggt	aac	tta	tca	gca	gtg	tca	tcc	tca	gaa	gga	aca	att	gaa	gaa	act	768
Gly	Asn	Leu	Ser	Ala 245	Val	Ser	Ser	Ser	Glu 250	Gly	Thr	Ile	Glu	Glu 255	Thr	
tta	aat	gaa	gct	tct	aaa	gag	ttg	cca	gag	agg	gca	aca	aat	cca	ttt	816
Leu	Asn	Glu	Ala 260	Ser	Lys	Glu	Leu	Pro 265	Glu	Arg	Ala	Thr	Asn 270	Pro	Phe	
gta	aat	aga	gat	tta	gca	gaa	ttt	tca	gaa	tta	gaa	tat	tca	gaa	atg	864
Val	Asn	Arg 275	Asp	Leu	Ala	Glu	Phe 280	Ser	Glu	Leu	Glu	Tyr 285	Ser	Glu	Met	
gga	tca	tct	ttt	aaa	ggc	tcc	cca	aaa	gga	gag	tca	gcc	ata	tta	gta	912
Gly	Ser 290	Ser	Phe	Lys	Gly	Ser 295	Pro	Lys	Gly	Glu	Ser 300	Ala	Ile	Leu	Val	
gaa	aac	act	aag	gaa	gaa	gta	att	gtg	agg	agt	aaa	gac	aaa	gag	gat	960
Glu	Asn	Thr	Lys	Glu	Glu 310	Val	Ile	Val	Arg	Ser 315	Lys	Asp	Lys	Glu	Asp 320	

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aaa gaa gac aga gtt gtg tct cca gaa aag aca atg gac att ttt aat	1056
Lys Glu Asp Arg 340 Val Val Ser Pro Glu 345 Lys Thr Met Asp Ile 350 Phe Asn	
gaa atg cag atg tca gta gta gca cct gtg agg gaa gag tat gca gac	1104
Glu Met Gln 355 Met Ser Val Val Ala 360 Pro Val Arg Glu 365 Tyr Ala Asp	
ttt aag cca ttt gaa caa gca tgg gaa gtg aaa gat act tat gag gga	1152
Phe Lys Pro Phe Glu Gln Ala 375 Trp Glu Val Lys Asp 380 Thr Tyr Glu Gly	
agt agg gat gtg ctg gct gct aga gct aat gtg gaa agt aaa gtg gac	1200
Ser Arg Asp Val Leu Ala 390 Ala Arg Ala Asn Val 395 Glu Ser Lys Val Asp 400	
aga aaa tgc ttg gaa gat agc ctg gag caa aaa agt ctt ggg aag gat	1248
Arg Lys Cys Leu Glu 405 Asp Ser Leu Glu Gln 410 Lys Ser Leu Gly Lys 415 Asp	
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Ser Glu Gly Arg 420 Asn Glu Asp Ala Ser 425 Phe Pro Ser Thr Pro 430 Glu Pro	
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Val Lys Asp Ser Ser Arg Ala Tyr 440 Ile Thr Cys Ala Ser 445 Phe Thr Ser	
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Ala Thr 450 Glu Ser Thr Thr Ala 455 Asn Thr Phe Pro Leu Leu Glu Asp His	
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Thr Ser Glu Asn Lys Thr 470 Asp Glu Lys Lys Ile 475 Glu Glu Arg Lys Ala 480	
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Gln Ile Ile Thr Glu 485 Lys Thr Ser Pro Lys 490 Thr Ser Asn Pro Phe 495 Leu	
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Val Ala Val Gln 500 Asp Ser Glu Ala Asp 505 Tyr Val Thr Thr Asp 510 Thr Leu	
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Ser Lys Val 515 Thr Glu Ala Ala Val 520 Ser Asn Met Pro Glu Gly Leu Thr	
cca gat tta gtt cag gaa gca tgt gaa agt gaa ctg aat gaa gcc aca	1632
Pro Asp Leu Val Gln Glu Ala 535 Cys Glu Ser Glu Leu 540 Asn Glu Ala Thr	
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Gly Thr Lys Ile Ala Tyr 550 Glu Thr Lys Val Asp 555 Leu Val Gln Thr Ser 560	
gaa gct ata caa gaa tca ctt tac ccc aca gca cag ctt tgc cca tca	1728
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ttt gag gaa gct gaa gca act ccg tca cca gtt ttg cct gat att gtt Phe Glu Glu Ala Glu Ala Thr Pro Ser Pro Val Leu Pro Asp Ile Val 580 585 590	1776
atg gaa gca cca tta aat tct ctc ctt cca agc gct ggt gct tct gta Met Glu Ala Pro Leu Asn Ser Leu Leu Pro Ser Ala Gly Ala Ser Val 595 600 605	1824
gtg cag ccc agt gta tcc cca ctg gaa gca cct cct cca gtt agt tat Val Gln Pro Ser Val Ser Pro Leu Glu Ala Pro Pro Val Ser Tyr 610 615 620	1872
gac agt ata aag ctt gag cct gaa aac ccc cca cca tat gaa gaa gcc Asp Ser Ile Lys Leu Glu Pro Glu Asn Pro Pro Tyr Glu Glu Ala 625 630 635 640	1920
atg aat gta gca cta aaa gct ttg gga aca aag gaa gga ata aaa gag Met Asn Val Ala Leu Lys Ala Leu Gly Thr Lys Glu Gly Ile Lys Glu 645 650 655	1968
cct gaa agt ttt aat gca gct gtt cag gaa aca gaa gct cct tat ata Pro Glu Ser Phe Asn Ala Ala Val Gln Glu Thr Glu Ala Pro Tyr Ile 660 665 670	2016
tcc att gcg tgt gat tta att aaa gaa aca aag ctc tcc act gag cca Ser Ile Ala Cys Asp Leu Ile Lys Glu Thr Lys Leu Ser Thr Glu Pro 675 680 685	2064
agt cca gat ttc tct aat tat tca gaa ata gca aaa ttc gag aag tcg Ser Pro Asp Phe Ser Asn Tyr Ser Glu Ile Ala Lys Phe Glu Lys Ser 690 695 700	2112
gtg ccc gaa cac gct gag cta gtg gag gat tcc tca cct gaa tct gaa Val Pro Glu His Ala Glu Leu Val Glu Asp Ser Ser Pro Glu Ser Glu 705 710 715 720	2160
cca gtt gac tta ttt agt gat gat tcg att cct gaa gtc cca caa aca Pro Val Asp Leu Phe Ser Asp Asp Ser Ile Pro Glu Val Pro Gln Thr 725 730 735	2208
caa gag gag gct gtg atg ctc atg aag gag agt ctc act gaa gtg tct Gln Glu Glu Ala Val Met Leu Met Lys Glu Ser Leu Thr Glu Val Ser 740 745 750	2256
gag aca gta gcc cag cac aaa gag gag aga ctt agt gcc tca cct cag Glu Thr Val Ala Gln His Lys Glu Glu Arg Leu Ser Ala Ser Pro Gln 755 760 765	2304
gag cta gga aag cca tat tta gag tct ttt cag ccc aat tta cat agt Glu Leu Gly Lys Pro Tyr Leu Glu Ser Phe Gln Pro Asn Leu His Ser 770 775 780	2352
aca aaa gat gct gca tct aat gac att cca aca ttg acc aaa aag gag Thr Lys Asp Ala Ala Ser Asn Asp Ile Pro Thr Leu Thr Lys Lys Glu 785 790 795 800	2400
aaa att tct ttg caa atg gaa gag ttt aat act gca att tat tca aat Lys Ile Ser Leu Gln Met Glu Glu Phe Asn Thr Ala Ile Tyr Ser Asn 805 810 815	2448
gat gac tta ctt tct tct aag gaa gac aaa ata aaa gaa agt gaa aca Asp Asp Leu Leu Ser Ser Lys Glu Asp Lys Ile Lys Glu Ser Glu Thr 815 820 825	2496

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825 830

820	ttt tca gat tca tct ccg att gag ata ata gat gaa ttt ccc acg ttt	2544
	Phe Ser Asp Ser Ser Pro Ile Glu Ile Ile Asp Glu Phe Pro Thr Phe	
	835 840 845	
	gtc agt gct aaa gat gat tct cct aaa tta gcc aag gag tac act gat	2592
	Val Ser Ala Lys Asp Asp Ser Pro Lys Leu Ala Lys Glu Tyr Thr Asp	
	850 855 860	
	cta gaa gta tcc gac aaa agt gaa att gct aat atc caa agc ggg gca	2640
	Leu Glu Val Ser Asp Lys Ser Glu Ile Ala Asn Ile Gln Ser Gly Ala	
	865 870 875 880	
	gat tca ttg cct tgc tta gaa ttg ccc tgt gac ctt tct ttc aag aat	2688
	Asp Ser Leu Pro Cys Leu Glu Leu Pro Cys Asp Leu Ser Phe Lys Asn	
	885 890 895	
	ata tat cct aaa gat gaa gta cat gtt tca gat gaa ttc tcc gaa aat	2736
	Ile Tyr Pro Lys Asp Glu Val His Val Ser Asp Glu Phe Ser Glu Asn	
	900 905 910	
	agg tcc agt gta tct aag gca tcc ata tcg cct tca aat gtc tct gct	2784
	Arg Ser Val Ser Lys Ala Ser Ile Ser Pro Ser Asn Val Ser Ala	
	915 920 925	
	ttg gaa cct cag aca gaa atg ggc agc ata gtt aaa tcc aaa tca ctt	2832
	Leu Glu Pro Gln Thr Glu Met Gly Ser Ile Val Lys Ser Lys Ser Leu	
	930 935 940	
	acg aaa gaa gca gag aaa aaa ctt cct tct gac aca gag aaa gag gac	2880
	Thr Lys Glu Ala Glu Lys Lys Leu Pro Ser Asp Thr Glu Lys Glu Asp	
	945 950 955 960	
	aga tcc ctg tca gct gta ttg tca gca gag ctg agt aaa act tca gtt	2928
	Arg Ser Leu Ser Ala Val Leu Ser Ala Glu Leu Ser Lys Thr Ser Val	
	965 970 975	
	gtt gac ctc ctc tac tgg aga gac att aag aag act gga gtg gtg ttt	2976
	Val Asp Leu Leu Tyr Trp Arg Asp Ile Lys Lys Thr Gly Val Val Phe	
	980 985 990	
	ggc gcc agc tta ttc ctg ctg ctg tct ctg aca gtg ttc agc att gtc	3024
	Gly Ala Ser Leu Phe Leu Leu Leu Ser Leu Thr Val Phe Ser Ile Val	
	995 1000 1005	
	agt gta acg gcc tac att gcc ttg gcc ctg ctc tcg gtg act atc	3069
	Ser Val Thr Ala Tyr Ile Ala Leu Ala Leu Leu Ser Val Thr Ile	
	1010 1015 1020	
	agc ttt agg ata tat aag ggc gtg atc cag gct atc cag aaa tca	3114
	Ser Phe Arg Ile Tyr Lys Gly Val Ile Gln Ala Ile Gln Lys Ser	
	1025 1030 1035	
	gat gaa ggc cac cca ttc agg gca tat tta gaa tct gaa gtt gct	3159
	Asp Glu Gly His Pro Phe Arg Ala Tyr Leu Glu Ser Glu Val Ala	
	1040 1045 1050	
	ata tca gag gaa ttg gtt cag aaa tac agt aat tct gct ctt ggt	3204
	Ile Ser Glu Glu Leu Val Gln Lys Tyr Ser Asn Ser Ala Leu Gly	
	1055 1060 1065	
	cat gtg aac agc aca ata aaa gaa ctg agg cgg ctt ttc tta gtt	3249

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His Val	Asn Ser Thr Ile	Lys	Glu Leu Arg Arg	Leu	Phe Leu Val	
1070		1075		1080		
gat gat	tta gtt gat tcc	ctg	aag ttt gca gtg	ttg	atg tgg gtg	3294
Asp Asp	Leu Val Asp Ser	Leu	Lys Phe Ala Val	Leu	Met Trp Val	
1085		1090		1095		
ttt act	tat gtt ggt gcc	ttg	ttc aat ggt ctg	aca	cta ctg att	3339
Phe Thr	Tyr Val Gly Ala	Leu	Phe Asn Gly Leu	Thr	Leu Leu Ile	
1100		1105		1110		
tta gct	ctg atc tca ctc	ttc	agt att cct gtt	att	tat gaa cgg	3384
Leu Ala	Leu Ile Ser Leu	Phe	Ser Ile Pro Val	Ile	Tyr Glu Arg	
1115		1120		1125		
cat cag	gtg cag ata gat	cat	tat cta gga ctt	gca	aac aag agt	3429
His Gln	Val Gln Ile Asp	His	Tyr Leu Gly Leu	Ala	Asn Lys Ser	
1130		1135		1140		
gtt aag	gat gcc atg gcc	aaa	atc caa gca aaa	atc	cct gga ttg	3474
Val Lys	Asp Ala Met Ala	Lys	Ile Gln Ala Lys	Ile	Pro Gly Leu	
1145		1150		1155		
aag cgc	aaa gca gat tga					3492
Lys Arg	Lys Ala Asp					
1160						

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<211> 1163

<212> PRT

<213> Rattus norvegicus

<400> 26

Met Glu Asp Ile	Asp Gln Ser Ser	Leu Val	Ser Ser Ser Thr	Asp Ser	
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Pro Pro Arg	Pro Pro Pro Ala	Phe Lys	Tyr Gln Phe Val	Thr Glu Pro	
	20	25		30	
Glu Asp Glu	Glu Asp Glu Glu	Glu Glu Glu	Asp Glu Glu	Glu Asp Asp	
	35	40		45	
Glu Asp Leu	Glu Glu Leu	Glu Val	Leu Glu Arg	Lys Pro Ala	Ala Gly
	50	55		60	
Leu Ser Ala	Ala Ala Val	Pro Pro Ala	Ala Ala Pro	Leu Leu Asp	
	65	70		75	80
Phe Ser Ser	Asp Ser Val	Pro Pro Ala	Pro Arg Gly	Pro Leu	Pro Ala
	85		90		95

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Ala Pro Pro Ala Ala Pro Glu Arg Gln Pro Ser Trp Glu Arg Ser Pro  
100 105 110

Ala Ala Pro Ala Pro Ser Leu Pro Pro Ala Ala Ala Val Leu Pro Ser  
115 120 125

Lys Leu Pro Glu Asp Asp Glu Pro Pro Ala Arg Pro Pro Pro Pro Pro  
130 135 140

Pro Ala Gly Ala Ser Pro Leu Ala Glu Pro Ala Ala Pro Pro Ser Thr  
145 150 155 160

Pro Ala Ala Pro Lys Arg Arg Gly Ser Gly Ser Val Asp Glu Thr Leu  
165 170 175

Phe Ala Leu Pro Ala Ala Ser Glu Pro Val Ile Pro Ser Ser Ala Glu  
180 185 190

Lys Ile Met Asp Leu Met Glu Gln Pro Gly Asn Thr Val Ser Ser Gly  
195 200 205

Gln Glu Asp Phe Pro Ser Val Leu Leu Glu Thr Ala Ala Ser Leu Pro  
210 215 220

Ser Leu Ser Pro Leu Ser Thr Val Ser Phe Lys Glu His Gly Tyr Leu  
225 230 235 240

Gly Asn Leu Ser Ala Val Ser Ser Ser Glu Gly Thr Ile Glu Glu Thr  
245 250 255

Leu Asn Glu Ala Ser Lys Glu Leu Pro Glu Arg Ala Thr Asn Pro Phe  
260 265 270

Val Asn Arg Asp Leu Ala Glu Phe Ser Glu Leu Glu Tyr Ser Glu Met  
275 280 285

Gly Ser Ser Phe Lys Gly Ser Pro Lys Gly Glu Ser Ala Ile Leu Val  
290 295 300

Glu Asn Thr Lys Glu Glu Val Ile Val Arg Ser Lys Asp Lys Glu Asp  
305 310 315 320

Leu Val Cys Ser Ala Ala Leu His Ser Pro Gln Glu Ser Pro Val Gly  
325 330 335

Lys Glu Asp Arg Val Val Ser Pro Glu Lys Thr Met Asp Ile Phe Asn  
340 345 350



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Glu Met Gln Met Ser Val Val Ala Pro Val Arg Glu Glu Tyr Ala Asp  
 355 360 365  
 Phe Lys Pro Phe Glu Gln Ala Trp Glu Val Lys Asp Thr Tyr Glu Gly  
 370 375 380  
 Ser Arg Asp Val Leu Ala Ala Arg Ala Asn Val Glu Ser Lys Val Asp  
 385 390 395 400  
 Arg Lys Cys Leu Glu Asp Ser Leu Glu Gln Lys Ser Leu Gly Lys Asp  
 405 410 415  
 Ser Glu Gly Arg Asn Glu Asp Ala Ser Phe Pro Ser Thr Pro Glu Pro  
 420 425 430  
 Val Lys Asp Ser Ser Arg Ala Tyr Ile Thr Cys Ala Ser Phe Thr Ser  
 435 440 445  
 Ala Thr Glu Ser Thr Thr Ala Asn Thr Phe Pro Leu Leu Glu Asp His  
 450 455 460  
 Thr Ser Glu Asn Lys Thr Asp Glu Lys Lys Ile Glu Glu Arg Lys Ala  
 465 470 475 480  
 Gln Ile Ile Thr Glu Lys Thr Ser Pro Lys Thr Ser Asn Pro Phe Leu  
 485 490 495  
 Val Ala Val Gln Asp Ser Glu Ala Asp Tyr Val Thr Thr Asp Thr Leu  
 500 505 510  
 Ser Lys Val Thr Glu Ala Ala Val Ser Asn Met Pro Glu Gly Leu Thr  
 515 520 525  
 Pro Asp Leu Val Gln Glu Ala Cys Glu Ser Glu Leu Asn Glu Ala Thr  
 530 535 540  
 Gly Thr Lys Ile Ala Tyr Glu Thr Lys Val Asp Leu Val Gln Thr Ser  
 545 550 555 560  
 Glu Ala Ile Gln Glu Ser Leu Tyr Pro Thr Ala Gln Leu Cys Pro Ser  
 565 570 575  
 Phe Glu Glu Ala Glu Ala Thr Pro Ser Pro Val Leu Pro Asp Ile Val  
 580 585 590  
 Met Glu Ala Pro Leu Asn Ser Leu Leu Pro Ser Ala Gly Ala Ser Val  
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595

600

605

Val Gln Pro Ser Val Ser Pro Leu Glu Ala Pro Pro Pro Val Ser Tyr  
 610 615 620

Asp Ser Ile Lys Leu Glu Pro Glu Asn Pro Pro Pro Tyr Glu Glu Ala  
 625 630 635 640

Met Asn Val Ala Leu Lys Ala Leu Gly Thr Lys Glu Gly Ile Lys Glu  
 645 650 655

Pro Glu Ser Phe Asn Ala Ala Val Gln Glu Thr Glu Ala Pro Tyr Ile  
 660 665 670

Ser Ile Ala Cys Asp Leu Ile Lys Glu Thr Lys Leu Ser Thr Glu Pro  
 675 680 685

Ser Pro Asp Phe Ser Asn Tyr Ser Glu Ile Ala Lys Phe Glu Lys Ser  
 690 695 700

Val Pro Glu His Ala Glu Leu Val Glu Asp Ser Ser Pro Glu Ser Glu  
 705 710 715 720

Pro Val Asp Leu Phe Ser Asp Asp Ser Ile Pro Glu Val Pro Gln Thr  
 725 730 735

Gln Glu Glu Ala Val Met Leu Met Lys Glu Ser Leu Thr Glu Val Ser  
 740 745 750

Glu Thr Val Ala Gln His Lys Glu Glu Arg Leu Ser Ala Ser Pro Gln  
 755 760 765

Glu Leu Gly Lys Pro Tyr Leu Glu Ser Phe Gln Pro Asn Leu His Ser  
 770 775 780

Thr Lys Asp Ala Ala Ser Asn Asp Ile Pro Thr Leu Thr Lys Lys Glu  
 785 790 795 800

Lys Ile Ser Leu Gln Met Glu Glu Phe Asn Thr Ala Ile Tyr Ser Asn  
 805 810 815

Asp Asp Leu Leu Ser Ser Lys Glu Asp Lys Ile Lys Glu Ser Glu Thr  
 820 825 830

Phe Ser Asp Ser Ser Pro Ile Glu Ile Ile Asp Glu Phe Pro Thr Phe  
 835 840 845

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Val Ser Ala Lys Asp Asp Ser Pro Lys Leu Ala Lys Glu Tyr Thr Asp  
 850 855 860

Leu Glu Val Ser Asp Lys Ser Glu Ile Ala Asn Ile Gln Ser Gly Ala  
 865 870 875 880

Asp Ser Leu Pro Cys Leu Glu Leu Pro Cys Asp Leu Ser Phe Lys Asn  
 885 890 895

Ile Tyr Pro Lys Asp Glu Val His Val Ser Asp Glu Phe Ser Glu Asn  
 900 905 910

Arg Ser Ser Val Ser Lys Ala Ser Ile Ser Pro Ser Asn Val Ser Ala  
 915 920 925

Leu Glu Pro Gln Thr Glu Met Gly Ser Ile Val Lys Ser Lys Ser Leu  
 930 935 940

Thr Lys Glu Ala Glu Lys Lys Leu Pro Ser Asp Thr Glu Lys Glu Asp  
 945 950 955 960

Arg Ser Leu Ser Ala Val Leu Ser Ala Glu Leu Ser Lys Thr Ser Val  
 965 970 975

Val Asp Leu Leu Tyr Trp Arg Asp Ile Lys Lys Thr Gly Val Val Phe  
 980 985 990

Gly Ala Ser Leu Phe Leu Leu Leu Ser Leu Thr Val Phe Ser Ile Val  
 995 1000 1005

Ser Val Thr Ala Tyr Ile Ala Leu Ala Leu Leu Ser Val Thr Ile  
 1010 1015 1020

Ser Phe Arg Ile Tyr Lys Gly Val Ile Gln Ala Ile Gln Lys Ser  
 1025 1030 1035

Asp Glu Gly His Pro Phe Arg Ala Tyr Leu Glu Ser Glu Val Ala  
 1040 1045 1050

Ile Ser Glu Glu Leu Val Gln Lys Tyr Ser Asn Ser Ala Leu Gly  
 1055 1060 1065

His Val Asn Ser Thr Ile Lys Glu Leu Arg Arg Leu Phe Leu Val  
 1070 1075 1080

Asp Asp Leu Val Asp Ser Leu Lys Phe Ala Val Leu Met Trp Val  
 1085 1090 1095

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Phe Thr Tyr Val Gly Ala Leu Phe Asn Gly Leu Thr Leu Leu Ile  
1100 1105 1110

Leu Ala Leu Ile Ser Leu Phe Ser Ile Pro Val Ile Tyr Glu Arg  
1115 1120 1125

His Gln Val Gln Ile Asp His Tyr Leu Gly Leu Ala Asn Lys Ser  
1130 1135 1140

Val Lys Asp Ala Met Ala Lys Ile Gln Ala Lys Ile Pro Gly Leu  
1145 1150 1155

Lys Arg Lys Ala Asp  
1160

<210> 27

<211> 25

<212> PRT

<213> Rattus norvegicus

<220>

<221> PEPTIDE

<222> (1)..(25)

<223> rat PEP4

<400> 27

Glu Glu Leu Val Gln Lys Tyr Ser Asn Ser Ala Leu Gly His Val Asn  
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Ser Thr Ile Lys Glu Leu Arg Arg Leu  
20 25

<210> 28

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> PRO/SER rich peptide

<220>

<221> PEPTIDE

<222> (1)..(17)

<223> Synthetic peptide

<400> 28

Pro Ser Ser Pro Pro Pro Ser Ser Pro Pro Pro Ser Ser Pro Pro Pro  
1 5 10 15

Ser

<210> 29

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> CA-NA-2F

<220>

<221> primer\_bind

<222> (1)..(25)

<223> CA-NA-2F primer

<400> 29

aagcaccatt gaattctgca gttcc

25

<210> 30

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> CA-NA-3R

<220>

<221> primer\_bind

<222> (1)..(28)

<223>

<400> 30  
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28

<210> 31

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> forward 5'

<220>

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<222> (1)..(33)

<223> forward primer

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33

<210> 32

<211> 27

<212> DNA

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<220>

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<223> reverse primer

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27

<210> 33

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<220>

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<223> primer

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29

<210> 34

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> reverse 5'-1

<220>

<221> primer\_bind

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<223> primer

<400> 34  
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28

<210> 35  
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 <223> 5' primer  
 <220>  
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 <222> (1)..(20)  
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<400> 35  
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20

<210> 36  
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 <220>  
 <221> primer\_bind  
 <222> (1)..(22)  
 <223> primer

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22

<210> 37  
 <211> 24  
 <212> DNA



<213> Artificial Sequence

<220>

<223> 3' primer

<220>

<221> primer\_bind

<222> (1)..(24)

<223> primer

<400> 37  
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24

<210> 38

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> 3' primer 2

<220>

<221> primer\_bind

<222> (1)..(22)

<223> primer

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22

<210> 39

<211> 28

<212> DNA

<213> Artificial Sequence

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<223> 5'-VL leader

<220>

<221> primer\_bind

<222> (1)..(28)

<223> primer

<400> 39  
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28

<210> 40

<211> 32

<212> DNA

<213> Artificial Sequence

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<223> 3'-ck

<220>

<221> primer\_bind

<222> (1)..(32)

<223> primer

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<212> DNA

<213> Artificial Sequence

<220>

<223> 5'-vH leader

<220>

<221> primer\_bind

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&lt;223&gt; primer

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31

&lt;210&gt; 42

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; 3'-CH hinge

&lt;220&gt;

&lt;221&gt; primer\_bind

&lt;222&gt; (1)..(24)

&lt;223&gt; primer

<400> 42  
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24

&lt;210&gt; 43

&lt;211&gt; 663

&lt;212&gt; DNA

&lt;213&gt; Mus musculus

&lt;220&gt;

&lt;221&gt; misc\_binding

&lt;222&gt; (1)..(663)

&lt;223&gt; DNA variable part of heavy chain 11C7

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gtagtctcag gattcgattt tagaagaaat tggatgagtt ggggccggca ggctcctggg 180

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aaagggctag aatggattgg agaaattaat ccagatagca gtaagataaa ctatacgcca	240
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gtgagcacag tgagatctga ggacacagcc ctttattact gtgtgagacc ggtctggatg	360
tatgctatgg actactgggg tcaaggaacc tcagtcaccg tctcctcagc caaaacgaca	420
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ctgggatgcc tgggtcaagg ctatttccct gagccagtga cagtgcactg gaactctgga	540
tccctgtcca gcggtgtgca caccttccca gctgtcctgc agtctgacct ctacactctg	600
agcagctcag tgactgtccc ctccagcacc tggcccagcg agaccgtcac ctgcaacgtt	660
gcc	663

<210> 44

<211> 717

<212> DNA

<213> Mus musculus

<220>

<221> misc\_binding

<222> (1)..(717)

<223> variable part of light chain of 11c7

<400> 44

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gttctgttga cccagactcc tctcactttg tcgataacca ttggacaacc agcctccatc	120
tcttgcaagt caagtcagag cctcttgcag agtgatggaa agacatattt gaattggttg	180
ttacagaggc caggccagtc tccaaagcgc ctaatctatc tgggtgtctaa actggactct	240
ggagtccctg acagggttcac tggcagtggga tcaggggacgg atttcacact gaaaatcagc	300
agagtggagg ctgaggattt gggactttat tattgctggc aaggtaacac ttttcctcag	360
acgttcggtg gaggcaccaa gctggaaatc aaacgggctg atgctgcacc aactgtatcc	420
atcttccac catccagtga gcagttaaca tctggaggtg cctcagtcgt gtgcttcttg	480
aacaacttct accccaaaga catcaatgtc aagtgggaaga ttgatggcag tgaacgacaa	540
aatggcgctc tgaacagttg gactgatcag gacagcaaag acagcaccta cagcatgagc	600
agcaccctca cgttgaccaa ggacgagtat gaacgacata acagctatac ctgtgaggcc	660
actcacaaga catcaacttc acccattgtc aagagcttca acaggggaga gtgttag	717

4-32761A\_UNZ.ST25.txt